<!--StartFragment-->RESULT 7
US-09-938-842A-1120
; Sequence 1120, Application US/09938842A
; Patent No. US20020160378A1
; GENERAL INFORMATION:
; APPLICANT: Harper, Jeff
; APPLICANT: Kreps, Joel
; APPLICANT: Wang, Xun
; APPLICANT: Zhu, Tong
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
; TITLE OF INVENTION: SAME, AND METHODS OF USE
; FILE REFERENCE: SCRIP1300-3
; CURRENT APPLICATION NUMBER: US/09/938,842A
; CURRENT FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: US 60/227,866
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: US 60/264,647
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/300,111
; PRIOR FILING DATE: 2001-06-22
; NUMBER OF SEQ ID NOS: 5379
; SEQ ID NO 1120
;   LENGTH: 1977
;   TYPE: DNA
;   ORGANISM: Arabidopsis thaliana
US-09-938-842A-1120

Alignment Scores:

Pred. No.:	1.12e-182	Length:	1977
Score:	1909.00	Matches:	356
Percent Similarity:	74.8%	Conservative:	115
Best Local Similarity:	56.5%	Mismatches:	117
Query Match:	53.7%	Indels:	42
DB:	3	Gaps:	7

US-10-544-180A-2 (1-673) x US-09-938-842A-1120 (1-1977)

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Qy          75 LeuPheSerLysGluIleLeuAspValIleAlaThrSerThrAlaAspLeuGlyProLeu 94
               |||   |||:::::::::   ::::::::::||||||   :::         |||   :::
Db         118 CTGTTATCTCAGGATGTG---AACATAGTTGCGACATACAGTGACCATTACGGCAATATA 174

Qy          95 SerLeuAspSerPheLysLysAsnAsnLeuSerAlaSerTrpArgGlyThrGlyValAsp 114
                  |||         |||      :::|||||   ||||||
Db         175 CGCCTTGGTAGGGTGAAAATGGGGGATCTTTCACCTTCTTGG------------------ 216

Qy         115 ProSerPheArgHisSerGluAsnProAla---------ThrProAspValLysSerAsn 131
                             ||||||||||||         :::         |||   :::
Db         217 ------------GTTTTGGAGAATCCTGCCTATCAAGTTAGCCGCAAAACAAAAGGTTCG 264

Qy         132 AsnLeuAsnGluLysArgAspSerIleSerLysAsp------------------------ 143
                  |||         |||||||||         |||
Db         265 CAGCTAGTTATACCACGGGATTCATTTCAAAATGATACTGGAATGGAAGATAATGCAAGC 324

Qy         144 ------SerIleHisGlnLysValGlu---------------------------------- 150
                    :::   :::|||      |||
Db         325 CATTCTACAACTAATCAGACTGATGAAAGCGAAAATCAGTTTCCAAACGTGGATTTTGCA 384

Qy         151 ThrProThrLysIleHisArgArgGlnLeuArgGluLysArgArgGluMetArgAlaAsn 170
               :::|||   |||:::   |||:::   ||||||::::::|||||      |||
Db         385 AGCCCAGCAAAACTGAAGCGGCAGATTTTACGTCAGGAAAGGAGAGGTCAACGAACTTTA 444
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Qy        171 GluLeuValGlnHisAsnAspAspThrIleLeuLysLeuGluAsnAlaAlaIleGluArg 190
              ||||||::::::         :::|||      :::::::::   |||||||||::::::
Db        445 GAGCTGATCCGACAAGAAAAGGAAACTGATGAGCAGATGCAAGAAGCAGCCATTCAGAAG 504

Qy        191 SerLysSerValAspSerAlaValLeuGlyLysTyrSerIleTrpArgArgGluAsnGlu 210
              |||   |||   :::::::::|||:::|||||||||||||||||||||||:::   |||
Db        505 TCAATGAGCTTTGAAAACTCAGTCATAGGGAAATACAGTATATGGAGGAGAGACTATGAG 564

Qy        211 AsnAspAsnSerAspSerAsnIleArgLeuMetArgAspGlnValIleMetAlaArgVal 230
              :::   |||:::|||:::   ::::::|||||||||||||||:::|||||||||:::
Db        565 AGCCCAAATGCTGATGCTATCTTGAAGCTTATGAGAGACCAGATCATAATGGCAAAAGCA 624

Qy        231 TyrSerGlyIleAlaLysLeuLysAsnLysAsnAspLeuLeuGlnGluLeuGlnAlaArg 250
              |||:::   |||||||||   ||||||      :::|||          |||      :::
Db        625 TATGCAAATATTGCCAAATCAAAAAATGTAACCAATCTGTACGTTTTCTTGATGCAGCAG 684

Qy        251 LeuLysAspSerGlnArgValLeuGlyGluAlaThrSerAspAlaAspLeuProArgSer 270
                  :::::::::||||||:::|||:::|||||||||||||||||||||||||   |||
Db        685 TGTGGAGAAAATAAACGTGTTATAGGTAAAGCAACCTCTGATGCTGACCTTCCTTCAAGC 744

Qy        271 AlaHisGluLysLeuArgAlaMetGlyGlnValLeuAlaLysAlaLysMetGlnLeuTyr 290
              |||   ::::::   :::||||||||||      |||:::   ||||||   :::||||||
Db        745 GCTCTTGATCAAGCAAAAGCCATGGGCCATGCACTCTCTCTTGCAAAAGACGAGTTATAT 804

Qy        291 AspCysLysLeuValThrGlyLysLeuArgAlaMetLeuGlnThrAlaAspGluGlnVal 310
              ||||||      :::      |||   ||||||:::|||||||:::   :::   :::|||
Db        805 GACTGCCATGAACTTGCAAAAAAGTTCCGGGCCATCCTTCAGTCCACTGAACGCAAAGTA 864

Qy        311 ArgSerLeuLysLysGlnSerThrPheLeuAlaGlnLeuAlaAlaLysThrIleProAsn 330
                  |||||||||:::   |||||||||   ||||||||||||||||||   |||
Db        865 GATGGACTGAAGAAAAAGGGAACCTTCTTAATTCAGCTAGCTGCCAAAACATTTCCCAAG 924

Qy        331 ProIleHisCysLeuSerMetArgLeuThrIleAspTyrTyrLeuLeuSerProGluLys 350
              |||:::|||||||||||||:::::::|||      ||||||:::::::|||         :::
Db        925 CCATTGCATTGCCTGAGTCTGCAGCTAGCGGCAGACTATTTTATTCTAGGTTTCAATGAA 984

Qy        351 ArgLysPheProArgSerGlu------------AsnLeuGluAsnProAsnLeuTyrHis 366
                        :::   :::                |||||||:::|||:::|||||||||
Db        985 GAGGATGCAGTGAAAGAGGATGTCAGTCAAAAGAAGCTTGAAGATCCTTCGCTCTATCAC 1044

Qy        367 TyrAlaLeuPheSerAspAsnValLeuAlaAlaSerValValValAsnSerThrIleMet 386
              ||||||:::|||||||||||||||||||||   |||||||||||||||||||||:::::::
Db       1045 TATGCGATCTTTTCGGATAACGTTCTGGCTACATCAGTGGTGGTGAACTCCACTGTCTTG 1104

Qy        387 AsnAlaLysAspProSerLysHisValPheHisLeuValThrAspLysLeuAsnPheGly 406
              |||||||||:::|||   :::|||||||||||||:::|||||||||||||||||||||||
Db       1105 AATGCAAAGGAACCGCAGAGGCATGTGTTCCATATAGTAACTGACAAACTGAATTTTGGT 1164

Qy        407 AlaMetAsnMetTrpPheLeuLeuAsnProProGlyLysAlaThrIleHisValGluAsn 426
              ||||||   |||||||||   :::|||   |||      |||||||||   |||||||||
Db       1165 GCAATGAAGATGTGGTTTCGCATCAATGCTCCTGCTGATGCGACGATTCAAGTTGAAAAC 1224

Qy        427 ValAspGluPheLysTrpLeuAsnSerSerTyrCysProValLeuArgGlnLeuGluSer 446
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Db       1225 ATAAATGATTTCAAGTGGCTGAACTCCTCTTACTGCTCTGTTCTACGGCAGCTTGAATCT 1284

Qy        447 AlaAlaMetArgGluTyrTyrPheLysAlaAspHisProThrSer---------GlySer 463
              |||   ::::::|||||||||||||||||||:::|||||||:::|||         |||:::
Db       1285 GCAAGGCTGAAAGAATACTATTTCAAAGCAAATCATCCTTCATCAATCTCAGCTGGCGCA 1344

Qy        464 SerAsnLeuLysTyrArgAsnProLysTyrLeuSerMetLeuAsnHisLeuArgPheTyr 483
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Db       1345 GATAATCTAAAGTACCGCAACCCAAAGTATCTATCGATGCTGAATCATCTCAGATTCTAC 1404

Qy        484 LeuProGluValTyrProLysLeuAsnLysIleLeuPheLeuAspAspAspIleIleVal 503
              |||||||||||||||||||||||    |||||||||||||||||||||||||||:::|||
Db       1405 CTTCCTGAGGTTTATCCGAAGCTGGAGAAGATTCTGTTTCTAGACGATGACATTGTGGTG 1464

Qy        504 GlnLysAspLeuThrProLeuTrpGluValAsnLeuAsnGlyLysValAsnGlyAlaVal 523
              ||||||||||||   ||||||||||||:::::::::   ||||||||||||||||||||
Db       1465 CAGAAGGACCTGGCACCACTATGGGAAATAGACATGCAAGGAAAAGTGAATGGTGCGGTG 1524

Qy        524 GluThrCysGlyGluSerPheHisArgPheAspLysTyrLeuAsnPheSerAsnProHis 543
              |||||||||   ||||||||||||||||||||||||||||||||||||||||||||||||
Db       1525 GAGACGTGCAAGGAGAGCTTCCACAGATTTGACAAGTACCTCAACTTCTCAAATCCAAAG 1584

Qy        544 IleAlaArgAsnPheAsnProAsnAlaCysGlyTrpAlaTyrGlyMetAsnMetPheAsp 563
              |||:::   |||||||:::      |||||||||||||||:::||||||||||||||||||
Db       1585 ATTTCAGAGAATTTTGACGCTGGTGCTTGTGGGTGGGCATTTGGGATGAATATGTTTGAC 1644

Qy        564 LeuLysGluTrpLysLysArgAspIleThrGlyIleTyrHisLysTrpGlnAsnMetAsn 583
              |||||||||||:::|||||||:::||||||||||||||||||   ||||||::::::|||
Db       1645 CTGAAAGAGTGGAGGAAACGGAACATTACAGGGATATATCACTATTGGCAAGACTTGAAT 1704

Qy        584 GluAsnArgThrLeuTrpLysLeuGlyThrLeuProProGlyLeuIleThrPheTyrGly 603
              |||:::|||||||||||||||||||:::||||||||||||||||||||||||||||||||
Db       1705 GAAGACAGAACACTGTGGAAGCTGGGATCGTTGCCACCGGGGCTGATAACATTTTACAAC 1764

Qy        604 LeuThrHisProLeuAsnLysAlaTrpHisValLeuGlyLeuGlyTyrAsnProSerIle 623
              |||||||:::   :::::::::::|||||||||||||||||||||||:::|||:::::::
Db       1765 CTGACGTATGCAATGGATAGGAGCTGGCACGTACTAGGGCTGGGATATGACCCAGCGCTA 1824

Qy        624 AspLysLysAspIleGluAsnAlaAlaValValHisTyrAsnGlyAsnMetLysProTrp 643
              ::::::      ||||||||||||||||||||||||||||||||||   |||||||||
Db       1825 AACCAAACAGCAATAGAGAATGCAGCGGTAGTGCATTACAATGGGAACTACAAGCCATGG 1884

Qy        644 LeuGluLeuAlaMetSerLysTyrArgProTyrTrpThrLysTyrIleLysPheAspHis 663
              |||   ||||||   :::|||||||:::|||||||||:::|||||||:::::::::|||:::
Db       1885 CTGGGTTTAGCATTCGCCAAGTACAAACCGTACTGGTCCAAGTACGTTGAGTACGACAAC 1944

Qy        664 ProTyrLeuArgArgCysAsnLeuHisGlu 673
              |||||||||||||||||:::::::::|||
Db       1945 CCTTATCTCCGACGGTGCGACATCAATGAA 1974

<!--EndFragment-->
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